

~~<110> Betenbaugh et al.~~

~~<120> Engineering Intracellular Sialylation Pathways~~

~~<130> PF509P2~~

~~<140> Unassigned
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~~<150> 60/227,579
<151> 2000-08-25~~

~~<150> 09/516,793
<151> 2000-03-01~~

~~<150> 60/169,624
<151> 1999-12-08~~

~~<150> 60/122,582
<151> 1999-03-02~~

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~~<170> PatentIn Ver. 2.1~~

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~~acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96
Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
20 25 30~~

~~tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144
Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
35 40 45~~

~~aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192
Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
50 55 60~~

~~cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240
Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
65 70 75 80~~

~~gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg 288
Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu~~

85

90

95

gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca 336
 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
 100 105 110

ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta 384
 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
 115 120 125

aag gaa gtg gct gct gcc cct gcc ctg cca ttt tat tac tat cac 432
 Lys Glu Val Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
 130 135 140

att cct gcc ttg aca ggg gta aag att cgt gct gag gag ttg ttg gat 480
 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
 145 150 155 160

ggg att ctg gat aag atc ccc acc ttc caa ggg ctg aaa ttc agt gat 528
 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
 165 170 175

aca gat ctc tta gac ttc ggg caa tgt gtt gat cag aat cgc cag caa 576
 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
 180 185 190

cag ttt gct ttc ctt ttt ggg gtg gat gag caa ctg ttg agt gct ctg 624
 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
 195 200 205

gtg atg gga gca act gga gca gtg ggc agt ttt gta tcc aga gat tta 672
 Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
 210 215 220

tca act ttg ttg tca aac tag gttttggagt gtcacagacc aaagccatca 723
 Ser Thr Leu Leu Ser Asn
 225 230

tgactctggc ctctgggatt ccaatgggcc cacccggct tccactgcag aaagcctcca 783

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caccttgaga cataatctac cttaaatagt gcattttt ctcagggaaat tttagatgaa 963

cttgaataaa ctctccttagc aaatgaaatc tcacaataag cattgaggta cctttgtga 1023

gccttaaaaa gtcttatttt gtgaaggggc aaaaactcta ggagtcacaa ctctcagtca 1083

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gttcctaat cctatttaa agttgtctaa ttttaaacca ctataatatg tcttcatttt 1263

aataaaatatt catttggaaat ctagaaaaac tctgagctac tgcatttagg caggcacttt 1323

aataccaaac tgtaacatgt ctcaactgta tacaactcaa aatacaccag ctcatttggc 1383
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 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 35 40 45
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 50 55 60
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
 65 70 75 80
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
 85 90 95
 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
 100 105 110
 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
 115 120 125
 Lys Glu Val Ala Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr His
 130 135 140
 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
 145 150 155 160
 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
 165 170 175
 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
 180 185 190
 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
 195 200 205
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 210 215 220
 Ser Thr Leu Leu Ser Asn
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1	5								10				15			
ggg	cga	ccg	tcc	cg	ggc	cg	ccg	ccg	aag	ctg	cag	cg	aac	tct	cg	96
Gly	Arg	Pro	Ser	Arg	Gly	Arg	Pro	Pro	Lys	Leu	Gln	Arg	Asn	Ser	Arg	
20	25								30							
ggc	ggc	cag	ggc	cga	gg	gt	gt	gag	aag	ccc	ccg	cac	ctg	gca	gcc	144
Gly	Gly	Gly	Gly	Gly	Arg	Gly	Val	Glu	Lys	Pro	Pro	His	Leu	Ala	Ala	Leu
35	40								45							
att	ctg	gcc	cg	gga	ggc	agc	aaa	ggc	atc	ccc	ctg	aag	aac	att	aag	192
Ile	Leu	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Pro	Leu	Lys	Asn	Ile	Lys	
50	55								60							
cac	ctg	gc	gg	gt	cc	ct	att	gg	tgg	gt	ct	cgt	gc	cc	ct	240
His	Leu	Ala	Gly	Val	Pro	Leu	Ile	Gly	Trp	Val	Leu	Arg	Ala	Ala	Leu	
65	70								75			80				
gat	tca	gg	gc	t	tc	c	c	ag	gt	tg	tc	ac	ga	ca	gt	288
Asp	Ser	Gly	Ala	Phe	Gln	Ser	Val	Trp	Val	Ser	Thr	Asp	His	Asp	Glu	
85									90			95				
att	gag	aat	gt	gc	aaa	caa	ttt	gg	gt	tc	ca	gt	ca	ag	ag	336
Ile	Glu	Asn	Val	Ala	Lys	Gln	Phe	Gly	Ala	Gln	Val	His	Arg	Arg	Ser	
100									105			110				
tct	gaa	gt	tca	aaa	gac	agc	tct	acc	tca	cta	gat	gc	atc	at	gaa	384
Ser	Glu	Val	Ser	Lys	Asp	Ser	Ser	Thr	Ser	Leu	Asp	Ala	Ile	Ile	Glu	
115									120			125				
ttt	ctt	aat	tat	yat	aat	gag	gk	gac	att	gt	ga	aa	at	aa	gt	432
Phe	Leu	Asn	Tyr	Xaa	Asn	Glu	Xaa	Asp	Ile	Val	Gly	Asn	Ile	Gln	Ala	
130									135			140				
act	tct	yca	tgt	tta	cat	cct	act	gat	ctt	caa	aaa	gtt	gc	ga	at	480
Thr	Ser	Xaa	Cys	Leu	His	Pro	Thr	Asp	Leu	Gln	Lys	Val	Ala	Glu	Met	
145									150			155			160	
att	cga	gaa	gaa	gga	ta	ta	gat	tct	gk	t	tc	gt	ga	cg	ca	528
Ile	Arg	Glu	Glu	Gly	Tyr	Asp	Ser	Xaa	Phe	Ser	Val	Val	Arg	Arg	His	

165

170

175

cag ttt cga tgg agt gaa att cag aaa gga gtt cgt gaa gtg acc gaa			576
Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu			
180	185	190	
cct ctg aat tta aat cca gct aaa cgg cct cgt cga caa gac tgg gat			624
Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp			
195	200	205	
gga gaa tta tat gaa aat ggc tca ttt tat ttt gct aaa aga cat ttg			672
Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu			
210	215	220	
ata gag atg ggt tac ttg cag ggt gga aaa tgg cat act acg aaa tgc			720
Ile Glu Met Gly Tyr Leu Gln Gly Lys Trp His Thr Thr Lys Cys			
225	230	235	240
gag ctg gaa cat agt gtg gat ata gat gtg gat att gat tgg cct att			768
Glu Leu Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile			
245	250	255	
gca gag caa aga gta tta aga tat ggc tat ttt ggc aaa gag aag ctt			816
Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu			
260	265	270	
aag gaa ata aaa ctt ttg gtt tgc aat att gat gga tgt ctc acc aat			864
Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn			
275	280	285	
ggc cac att tat gta tca gga gac caa aaa gaa ata ata tct tat gat			912
Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp			
290	295	300	
gta aaa gat gct att ggg ata agt tta tta aag aaa agt ggt att gag			960
Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu			
305	310	315	320
gtg agg cta atc tca gaa agg gcc tgt tca aag cag acg ctg tct tct			1008
Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser			
325	330	335	
tta aaa ctg gat tgc aaa atg gaa gtc agt gta tca gac aag cta gca			1056
Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala			
340	345	350	
gtt gta gat gaa tgg aga aaa gaa atg ggc ctg tgc tgg aaa gaa gtg			1104
Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val			
355	360	365	
gca tat ctt gga aat gaa gtg tct gat gaa gag tgc ttg aag aga gtg			1152
Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val			
370	375	380	
ggc cta agt ggc gct cct gct gat gcc tgt tcc tac gcc cag aag gct			1200
Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala			
385	390	395	400

gtt gga tac att tgc aaa tgt aat ggt ggc cgt ggt gcc atc cga gaa 1248
 Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu
 405 410 415

ttt gca gag cac att tgc cta cta atg gaa aaa gtt aat aat tca tgc 1296
 Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys
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 Gln Lys

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 Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu
 35 40 45
 Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
 50 55 60
 His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
 65 70 75 80
 Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
 85 90 95
 Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
 100 105 110
 Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu
 115 120 125
 Phe Leu Asn Tyr Xaa Asn Glu Xaa Asp Ile Val Gly Asn Ile Gln Ala
 130 135 140
 Thr Ser Xaa Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
 145 150 155 160

Ile Arg Glu Glu Gly Tyr Asp Ser Xaa Phe Ser Val Val Arg Arg His
 165 170 175
 Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu
 180 185 190
 Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp
 195 200 205
 Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu
 210 215 220
 Ile Glu Met Gly Tyr Leu Gln Gly Lys Trp His Thr Thr Lys Cys
 225 230 235 240
 Glu Leu Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile
 245 250 255
 Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu
 260 265 270
 Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn
 275 280 285
 Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp
 290 295 300
 Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu
 305 310 315 320
 Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser
 325 330 335
 Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala
 340 345 350
 Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val
 355 360 365
 Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val
 370 375 380
 Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala
 385 390 395 400
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 405 410 415
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 Gln Lys

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 cac ccg tgc ttc atc att gcc gag atc ggc cag aac cac cag ggc gac 96
 His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp
 20 25 30
 ctg gac gta gcc aag cgc atg atc cgc atg gcc aag gag tgt ggg gct 144
 Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala

35

40

45

gat tgt gcc aag ttc cag aag agt gag cta gaa ttc aag ttt aat cgg	192
Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg	
50 55 60	
aaa gcc ttg gag agg cca tac acc tcg aag cat tcc tgg ggg aag acg	240
Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr	
65 70 75 80	
tac ggg gag cac aaa cga cat ctg gag ttc agc cat gac cag tac agg	288
Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg	
85 90 95	
gag ctg cag agg tac gcc gag gag gtt ggg atc ttc ttc act gcc tct	336
Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser	
100 105 110	
ggc atg gat gag atg gca gtt gaa ttc ctg cat gaa ctg aat gtt cca	384
Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro	
115 120 125	
ttt ttc aaa gtt gga tct gga gac act aat aat ttt cct tat ctg gaa	432
Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu	
130 135 140	
aag aca gcc aaa aaa ggt cgc cca atg gtg atc tcc agt ggg atg cag	480
Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln	
145 150 155 160	
tca atg gac acc atg aag caa gtt tat cag atc gtg aag ccc ctc aac	528
Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn	
165 170 175	
ccc aac ttc tgc ttc ttg cag tgt acc agc gca tac ccg ctc cag cct	576
Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro	
180 185 190	
gag gac gtc aac ctg cgg gtc atc tcg gaa tat cag aag ctc ttt cct	624
Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro	
195 200 205	
gac att ccc ata ggg tat tct ggg cat gaa aca ggc ata gcg ata tct	672
Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser	
210 215 220	
gtg gcc gca gtg gct ctg ggg gcc aag gtg ttg gaa cgt cac ata act	720
Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr	
225 230 235 240	
ttg gac aag acc tgg aag ggg agt gac cac tcg gcc tcg ctg gag cct	768
Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro	
245 250 255	
gga gaa ctg gcc gag ctg gtg cgg tca gtg cgt ctt gtg gag cgt gcc	816
Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala	
260 265 270	

ctg ggc tcc cca acc aag cag ctg ctg ccc tgc gag atg gcc tgc aat	864
Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn	
275 280 285	
gag aag ctg ggc aag tct gtg gtg gcc aaa gtg aaa att ccg gaa ggc	912
Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly	
290 295 300	
acc att cta aca atg gac atg ctc acc gtg aag gtg ggt gag ccc aaa	960
Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys	
305 310 315 320	
gcc tat cct cct gaa gac atc ttt aat cta gtg ggc aag aag gtc ctg	1008
Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu	
325 330 335	
gtc act gtt gaa gag gat gac acc atc atg gaa gaa ttg gta gat aat	1056
Val Thr Val Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn	
340 345 350	
cat ggc aaa aaa atc aag tct taa	1080
His Gly Lys Lys Ile Lys Ser	
355	

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Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala	
35 40 45	
Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg	
50 55 60	
Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr	
65 70 75 80	
Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg	
85 90 95	
Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser	
100 105 110	
Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro	
115 120 125	
Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu	
130 135 140	
Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln	
145 150 155 160	
Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn	
165 170 175	
Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro	
180 185 190	
Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro	
195 200 205	
Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser	

210	215	220	
Val Ala Ala Val Ala Leu Gly Ala Lys Val	Leu Glu Arg His Ile Thr		
225	230	235	
Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser	Leu Glu Pro	240	
245	250	255	
Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val	Glu Arg Ala		
260	265	270	
Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn			
275	280	285	
Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly			
290	295	300	
Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys			
305	310	315	320
Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu			
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340	345	350	
His Gly Lys Lys Ile Lys Ser			
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<212> DNA

<213> Escherichia coli

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<222> (1)..(1041)

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agt gtt gat att gca aga gaa atg ata tta aaa gcc aaa gag gcc ggt	96		
Ser Val Asp Ile Ala Arg Glu Met Ile Leu Lys Ala Lys Glu Ala Gly			
20	25	30	

gtt aat gca gta aaa ttc caa aca ttt aaa gct gat aaa tta att tca	144		
Val Asn Ala Val Lys Phe Gln Thr Phe Lys Ala Asp Lys Leu Ile Ser			
35	40	45	

gct att gca cct aag gca gag tat caa ata aaa aac aca gga gaa tta	192		
Ala Ile Ala Pro Lys Ala Glu Tyr Gln Ile Lys Asn Thr Gly Glu Leu			
50	55	60	

gaa tct cag tta gaa atg aca aaa aag ctt gaa atg aag tat gac gat	240		
Glu Ser Gln Leu Glu Met Thr Lys Lys Leu Glu Met Lys Tyr Asp Asp			
65	70	75	80

tat ctc cat cta atg gaa tat gca gtc agt tta aat tta gat gtt ttt	288		
Tyr Leu His Leu Met Glu Tyr Ala Val Ser Leu Asn Leu Asp Val Phe			
85	90	95	

tct acc cct ttt gac gaa gac tct att gat ttt tta gca tct ttg aaa	336
Ser Thr Pro Phe Asp Glu Asp Ser Ile Asp Phe Leu Ala Ser Leu Lys	

100	105	110	
caa aaa ata tgg aaa atc cct tca ggt gag tta ttg aat tta ccg tat Gln Lys Ile Trp Lys Ile Pro Ser Gly Glu Leu Leu Asn Leu Pro Tyr 115 120 125			384
ctt gaa aaa ata gcc aag ctt ccg atc cct gat aag aaa ata atc ata Leu Glu Lys Ile Ala Lys Leu Pro Ile Pro Asp Lys Lys Ile Ile Ile 130 135 140			432
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ttt ata aat aat aaa gtt ccg gtt ggt aat 'att aca ata tta cat tgc Phe Ile Asn Asn Lys Val Pro Val Gly Asn Ile Thr Ile Leu His Cys 165 170 175			528
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aat gat ttg aaa aaa cac ttc cct aag aat aac ata ggc ttc tct gat Asn Asp Leu Lys Lys His Phe Pro Lys Asn Asn Ile Gly Phe Ser Asp 195 200 205			624
cat tct agc ggg ttt tat gca gct att gcg gcg gtg cct tat gga ata His Ser Ser Gly Phe Tyr Ala Ala Ala Val Pro Tyr Gly Ile 210 215 220			672
act ttt att gaa aaa cat ttc act tta gat aaa tct atg tct ggc cca Thr Phe Ile Glu Lys His Phe Thr Leu Asp Lys Ser Met Ser Gly Pro 225 230 235 240			720
gat cat ttg gcc tca ata gaa cct gat gaa ctg aaa cat ctt tgt att Asp His Leu Ala Ser Ile Glu Pro Asp Glu Leu Lys His Leu Cys Ile 245 250 255			768
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 35 40 45
 Ala Ile Ala Pro Lys Ala Glu Tyr Gln Ile Lys Asn Thr Gly Glu Leu
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 Glu Ser Gln Leu Glu Met Thr Lys Lys Leu Glu Met Lys Tyr Asp Asp
 65 70 75 80
 Tyr Leu His Leu Met Glu Tyr Ala Val Ser Leu Asn Leu Asp Val Phe
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 Ser Thr Pro Phe Asp Glu Asp Ser Ile Asp Phe Leu Ala Ser Leu Lys
 100 105 110
 Gln Lys Ile Trp Lys Ile Pro Ser Gly Glu Leu Leu Asn Leu Pro Tyr
 115 120 125
 Leu Glu Lys Ile Ala Lys Leu Pro Ile Pro Asp Lys Lys Ile Ile Ile
 130 135 140
 Ser Thr Gly Met Ala Thr Ile Asp Glu Ile Lys Gln Ser Val Ser Ile
 145 150 155 160
 Phe Ile Asn Asn Lys Val Pro Val Gly Asn Ile Thr Ile Leu His Cys
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 Asn Thr Glu Tyr Pro Thr Pro Phe Glu Asp Val Asn Leu Asn Ala Ile
 180 185 190
 Asn Asp Leu Lys Lys His Phe Pro Lys Asn Asn Ile Gly Phe Ser Asp
 195 200 205
 His Ser Ser Gly Phe Tyr Ala Ala Ile Ala Val Pro Tyr Gly Ile
 210 215 220
 Thr Phe Ile Glu Lys His Phe Thr Leu Asp Lys Ser Met Ser Gly Pro
 225 230 235 240
 Asp His Leu Ala Ser Ile Glu Pro Asp Glu Leu Lys His Leu Cys Ile
 245 250 255
 Gly Val Arg Cys Val Glu Lys Ser Leu Gly Ser Asn Ser Lys Val Val
 260 265 270
 Thr Ala Ser Glu Arg Lys Asn Lys Ile Val Ala Arg Lys Ser Ile Ile
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 Ile Lys Thr Glu Ile Lys Lys Gly Glu Val Phe Ser Glu Lys Asn Ile
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 Thr Thr Lys Arg Pro Gly Asn Gly Ile Ser Pro Met Glu Trp Tyr Asn
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 Leu Leu Gly Lys Ile Ala Glu Gln Asp Phe Ile Pro Asp Glu Leu Ile
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